

vyi (in varieties *Lüina*, *Torcione Nero*, *Marrone Michelangelo*, *Marrone Lattecaldo* and *Bouche de Bétizac*), as well as two of 41 shoots from seed chestnuts (*Lüina* and *Bouche de Bétizac*), and two of 17 rootstocks (*Lüina* and *Torcione Nero* varieties). For 112 samples from 56 rootstock/graft pairs, *G. smithogilvyi* was found in 12% of the rootstocks and 60% of the grafts. These results showed low incidence of *G. smithogilvyi* in rootstock propagation material, and high contamination of grafting material in all varieties, and confirm that *G. smithogilvyi* is an endophyte.

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Characterization of *Elsinoë ampelina*, the causal agent of grapevine anthracnose in Brazil. R.F. SANTOS, M. CIAMPI-GUILLARDI, L. AMORIM, N. S. MASSOLA JÚNIOR, M. B SPÓSITO. *Departamento de Fitopatologia e Nematologia, Escola Superior de Agricultura “Luiz de Queiroz”, Universidade de São Paulo, 13418-900 Piracicaba, SP, Brazil. E-mail: ricardofeliciano@usp.br*

Anthracnose, caused by *Elsinoë ampelina*, is an important disease in vineyards in South and Southeast Brazil, the main grape-producing regions in the country. This study characterized *E. ampelina* isolates associated with grapevine anthracnose in Brazil through molecular analysis, morphological characterization and pathogenicity tests. Thirty-nine *E. ampelina* isolates were obtained from leaves, stems and berries with anthracnose symptoms collected in the Rio Grande do Sul and São Paulo States. Fungus characterization was carried out using molecular analysis based on ITS, TEF 1- α and HIS3 regions, in combination with cultural and conidial morphology. For pathogenicity tests, ten isolates were inoculated onto *Vitis labrusca* cv. Niagara Rosada. ITS sequences showed only two polymorphic sites within the 602 bp sequenced and TEF 1- α sequences were monomorphic. However, HIS3 was the most informative region showing 55 polymorphic sites. Haplotype network analysis based on multilocus alignment (ITS, TEF 1- α and HIS3) grouped the isolates into seven haplotypes. Colonies of *E. ampelina* isolates showed slow growth (23 to 28 mm diam. at 30 d), variable colouration and wrinkled texture on PDA medium.

Conidia were cylindrical to oblong with rounded ends, hyaline, aseptate, 3.6 to 7.0 μ m long and 2.0 to 3.4 μ m wide. Inoculations on ‘Niagara Rosada’ confirmed the pathogenicity of all isolates inoculated. These caused reductions of shoot dry weight by up to 80%, and severity of leaf disease reached a maximum of 72%.

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Genetic and phenotypic diversity of *Verticillium dahliae* populations from sunflower in Europe.

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The incidence of *Verticillium dahliae* (*Vd*) affecting sunflower in France, Italy, Spain and countries around Black Sea has greatly increased in the last five years, becoming a major constraint for sunflower production in some regions. Twenty Isolates of *Vd* collected in these countries, and one from Argentina, were characterized under a multidisciplinary study. The isolates were inoculated, by root immersion in suspensions of conidia, to seven sunflower genotypes with different phenotypic responses according to previous experiments. Some of the isolates were also inoculated onto different hosts (artichoke, eggplant, cotton, tomato and lettuce) to determine the host pathogenicity spectrum of *Vd* from sunflower. The vegetative compatibility groups (VCGs) were determined through complementation between nit mutants of the fungal isolates and VCG reference strains. Phenotypic and genetic data indicated that the isolates from Black Sea countries were distinguishable from those from West Europe and Argentina, which could be due to the presence of at least two different races. Artichoke was very susceptible to all the isolates and significant crop \times *Vd* isolate interactions were found for disease variables. Ongoing experiments using SSR reference markers for *Vd* will provide extensive information about the molecular structure of populations from sunflower and the re-

relationships with populations from other crops. This study is the first attempt to increase understanding of the genetics, virulence and phenotypic characteristics of the *Vd* isolates affecting sunflower in Europe.

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Identification of two species belonging of *Polerovirus* in hot pepper (*Capsicum* spp.) in Italy: a new phytosanitary risk. A. TIBERINI¹, I. ADAMS², A. FOX², A. FOWKES², S. DAVINO³, L. TOMASSOLI⁴. ¹Università degli Studi “Mediterranea” di Reggio Calabria, Feo di Vito, 89121 Reggio Calabria (RC) Italy. ²Food and Environmental Research Agency (FERA), Sand Hutton, York, UK. ³Università degli Studi di Palermo, Dipartimento Scienze Agrarie e Forestali, Viale delle Scienze ED. 5, 90128 Palermo, Italy. ⁴Consiglio per la ricerca in agricoltura e l’analisi dell’economia agraria, Centro di ricerca per la patologia vegetale, Via C.G. Bertero 22, 00156 Roma, Italy. E-mail: antonio.tiberini@unirc.it

Diseases caused by aphid-borne poleroviruses (genus *Polerovirus*, family *Luteoviridae*) are emerging threats to the production of important crops. During the current decade, several first outbreak and survey studies have been reported for poleroviruses in *Capsicum annuum*. In Italy, two simultaneous detections of *Pepper vein yellows virus* (PeVYV) occurred in 2015 in central Italy (Lazio) in hot pepper in open fields, and southern Italy (Sicily) in greenhouse-grown sweet pepper. During recent investigations, hot pepper has been found affected by multiple viruses, causing a range of symptoms including leaf yellowing, brittleness, crinkling, mosaic and necrosis. Most of the viruses were endemic (*Tomato spotted wilt virus*, *Alfalfa mosaic virus*, *Broad bean wilt virus 2*, *Potato virus Y*, *Pepper mild mottle virus*) but *Chilli veinal mottle virus* (ChiVMV) and PeVYV were new for Italy. The concern that other alien viruses could be introduced through intensive but free exchange and trade of foreign germplasm has led to the use the NGS technique to analyse the whole *viroma* of some severely symptomatic chilli plants of other *Capsicum* spp. A new isolate has been identified sharing high nucleotide sequence similarity with the putative species *Pepper yellow leaf curl virus* (PYCV) in the genus *Polerovirus*, for which taxonomy is under debate

to be considered as new species or a PeVYV strain. On the basis of preliminary partial genome analysis, this isolate showed a mosaic sequence related to PeVYV and *Tobacco vein distorting virus* as previously reported in the first PYCV outbreak in Israel. This study aims to clarify the taxonomic position of this putative Polerovirus.

Range of expansion and genetic diversity of *Bemisia tabaci* populations in Italy, under the recent threat of *Tomato leaf curl New Delhi virus* spread. S. BERTIN¹, G. PARRELLA², M. GIORGINI², M. NANNINI³, S. DAVINO⁴, M. LUIGI¹ and L. TOMASSOLI¹. ¹Consiglio per la ricerca in agricoltura e l’analisi dell’economia agraria, Centro di ricerca Difesa e Certificazione (CREA-DC), Via C.G. Bertero 22 - 00156 Roma, Italy. ²Consiglio Nazionale delle Ricerche, Istituto per la Protezione Sostenibile delle Piante (CNR-IPSP), Sede di Portici, via Università 133, Portici, Napoli, Italy. ³Agris Sardegna, Servizio Ricerca Studi ambientali, Difesa delle colture e Qualità delle produzioni, Viale Trieste 111 - 09123 Cagliari, Italy. ⁴Università degli Studi di Palermo, Dipartimento Scienze Agrarie e Forestali, Viale delle Scienze ED. 5 - 90128 Palermo, Italy. E-mail: sabrina.ber-tin@crea.gov.it

After the introduction of *Tomato leaf curl New Delhi virus* (ToLCNDV; *Begomovirus*: *Geminiviridae*), the insect vector *Bemisia tabaci* (Hemiptera: Aleyrodidae) strengthens its harmfulness to the horticultural crops in the Mediterranean basin. Within the *B. tabaci* complex, Mediterranean (Med) and Middle East–Asia Minor 1 (MEAM1) species (formerly referred to as biotypes Q and B) are widespread in the endangered areas, and are regarded as the main vectors responsible for ToLCNDV transmission. In Italy, *B. tabaci* has raised the status of the virus in warm areas, including the southern regions, Sicily and Sardinia, and the north-western coast (Liguria). During the last decade, the level of Med populations has progressively increased, and Med displaced MEAM1 in those areas where intensive farming occurs. Following ToLCNDV outbreaks in Italy, surveys were carried out to investigate the infestations of *B. tabaci* in the affected areas. ToLCNDV-associated Med populations of *B. tabaci* were found to be established in the Lazio region (central Italy), where begomovirus epidemics had never occurred and vector presence was thought to be only occasional. Nevertheless, single and mixed